

SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Screening Method

<130> P04-080PCT

<150> JP 2002-3769

<151> 2002-01-10

<160> 11

<170> PatentIn version 3.1

<210> 1

<211> 123

<212> PRT

<213> Homo .sapiens

<220>

<221> MISC_FEATURE

<223> Partial amino acid sequence of Egr-1 protein which is conserved between human, mouse and rat.

<400> 1

```

Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg Met Arg Lys Tyr Pro Asn
1          5          10          15
Arg Pro Ser Lys Thr Pro Pro His Glu Arg Pro Tyr Ala Cys Pro Val
          20          25          30
Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser Asp Glu Leu Thr Arg His
          35          40          45
Ile Arg Ile His Thr Gly Gln Lys Pro Phe Gln Cys Arg Ile Cys Met
          50          55          60
Arg Asn Phe Ser Arg Ser Asp His Leu Thr Thr His Ile Arg Thr His
65          70          75          80
Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile Cys Gly Arg Lys Phe Ala
          85          90          95
Arg Ser Asp Glu Arg Lys Arg His Thr Lys Ile His Leu Arg Gln Lys
          100          105          110
Asp Lys Lys Ala Asp Lys Ser Val Val Ala Ser
          115          120

```

<210> 2

<211> 543

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1          5          10          15
Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
          20          25          30
Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
          35          40          45
Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
          50          55          60
Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser
65          70          75          80
Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro
          85          90          95
Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn
          100          105          110
Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu

```

04080seq.txt

```

115      120      125
Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn
130      135      140
Ser Gly Asn Thr Leu Trp Pro Glu Pro Leu Phe Ser Leu Val Ser Gly
145      150      155      160
Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser
165      170      175
Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys
180      185      190
Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr
195      200      205
Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala
210      215      220
Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr
225      230      235      240
Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu
245      250      255
Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys
260      265      270
Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro
275      280      285
Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu
290      295      300
Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg
305      310      315      320
Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg
325      330      335
Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
340      345      350
Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
355      360      365
Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
370      375      380
Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385      390      395      400
Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys
405      410      415
Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
420      425      430
Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
435      440      445
Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
450      455      460
Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
465      470      475      480
Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
485      490      495
Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
500      505      510
Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
515      520      525
Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
530      535      540

```

<210> 3
 <211> 1629
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1629)
 <223>

04080seq.txt

<400> 3

atg gcc gcg gcc aag gcc gag atg cag ctg atg tcc ccg ctg cag atc	48
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile	
1 5 10 15	
tct gac ccg ttc gga tcc ttt cct cac tcg ccc acc atg gac aac tac	96
Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr	
20 25 30	
cct aag ctg gag gag atg atg ctg ctg agc aac ggg gct ccc cag ttc	144
Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe	
35 40 45	
ctc ggc gcc gcc ggg gcc cca gag ggc agc ggc agc aac agc agc agc	192
Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser	
50 55 60	
agc agc agc ggg ggc ggt gga ggc ggc ggg ggc ggc agc aac agc agc	240
Ser Ser Ser Gly Gly Gly Gly Gly Gly Gly Gly Gly Ser Asn Ser Ser	
65 70 75 80	
agc agc agc agc acc ttc aac cct cag gcg gac acg ggc gag cag ccc	288
Ser Ser Ser Ser Thr Phe Asn Pro Gln Ala Asp Thr Gly Glu Gln Pro	
85 90 95	
tac gag cac ctg acc gca gag tct ttt cct gac atc tct ctg aac aac	336
Tyr Glu His Leu Thr Ala Glu Ser Phe Pro Asp Ile Ser Leu Asn Asn	
100 105 110	
gag aag gtg ctg gtg gag acc agt tac ccc agc caa acc act cga ctg	384
Glu Lys Val Leu Val Glu Thr Ser Tyr Pro Ser Gln Thr Thr Arg Leu	
115 120 125	
ccc ccc atc acc tat act ggc cgc ttt tcc ctg gag cct gca ccc aac	432
Pro Pro Ile Thr Tyr Thr Gly Arg Phe Ser Leu Glu Pro Ala Pro Asn	
130 135 140	
agt ggc aac acc ttg tgg ccc gag ccc ctc ttc agc ttg gtc agt ggc	480
Ser Gly Asn Thr Leu Trp Pro Glu Pro Leu Phe Ser Leu Val Ser Gly	
145 150 155 160	
cta gtg agc atg acc aac cca ccg gcc tcc tcg tcc tca gca cca tct	528
Leu Val Ser Met Thr Asn Pro Pro Ala Ser Ser Ser Ser Ala Pro Ser	
165 170 175	
cca gcg gcc tcc tcc gcc tcc gcc tcc cag agc cca ccc ctg agc tgc	576
Pro Ala Ala Ser Ser Ala Ser Ala Ser Gln Ser Pro Pro Leu Ser Cys	
180 185 190	
gca gtg cca tcc aac gac agc agt ccc att tac tca gcg gca ccc acc	624
Ala Val Pro Ser Asn Asp Ser Ser Pro Ile Tyr Ser Ala Ala Pro Thr	
195 200 205	
ttc ccc acg ccg aac act gac att ttc cct gag cca caa agc cag gcc	672
Phe Pro Thr Pro Asn Thr Asp Ile Phe Pro Glu Pro Gln Ser Gln Ala	
210 215 220	
ttc ccg ggc tcg gca ggg aca gcg ctc cag tac ccg cct cct gcc tac	720
Phe Pro Gly Ser Ala Gly Thr Ala Leu Gln Tyr Pro Pro Pro Ala Tyr	
225 230 235 240	
cct gcc gcc aag ggt ggc ttc cag gtt ccc atg atc ccc gac tac ctg	768
Pro Ala Ala Lys Gly Gly Phe Gln Val Pro Met Ile Pro Asp Tyr Leu	
245 250 255	
ttt cca cag cag cag ggg gat ctg ggc ctg ggc acc cca gac cag aag	816
Phe Pro Gln Gln Gln Gly Asp Leu Gly Leu Gly Thr Pro Asp Gln Lys	
260 265 270	
ccc ttc cag ggc ctg gag agc cgc acc cag cag cct tcg cta acc cct	864
Pro Phe Gln Gly Leu Glu Ser Arg Thr Gln Gln Pro Ser Leu Thr Pro	
275 280 285	
ctg tct act att aag gcc ttt gcc act cag tcg ggc tcc cag gac ctg	912
Leu Ser Thr Ile Lys Ala Phe Ala Thr Gln Ser Gly Ser Gln Asp Leu	
290 295 300	
aag gcc ctc aat acc agc tac cag tcc cag ctc atc aaa ccc agc cgc	960
Lys Ala Leu Asn Thr Ser Tyr Gln Ser Gln Leu Ile Lys Pro Ser Arg	
305 310 315 320	
atg cgc aag tat ccc aac cgg ccc agc aag acg ccc ccc cac gaa cgc	1008
Met Arg Lys Tyr Pro Asn Arg Pro Ser Lys Thr Pro Pro His Glu Arg	
325 330 335	

04080seq.txt

```

cct tac gct tgc cca gtg gag tcc tgt gat cgc cgc ttc tcc cgc tcc 1056
Pro Tyr Ala Cys Pro Val Glu Ser Cys Asp Arg Arg Phe Ser Arg Ser
340 345 350
gac gag ctc acc cgc cac atc cgc atc cac aca ggc cag aag ccc ttc 1104
Asp Glu Leu Thr Arg His Ile Arg Ile His Thr Gly Gln Lys Pro Phe
355 360 365
cag tgc cgc atc tgc atg cgc aac ttc agc cgc agc gac cac ctc acc 1152
Gln Cys Arg Ile Cys Met Arg Asn Phe Ser Arg Ser Asp His Leu Thr
370 375 380
acc cac atc cgc acc cac aca ggc gaa aag ccc ttc gcc tgc gac atc 1200
Thr His Ile Arg Thr His Thr Gly Glu Lys Pro Phe Ala Cys Asp Ile
385 390 395 400
tgt gga aga aag ttt gcc agg agc gat gaa cgc aag agg cat acc aag 1248
Cys Gly Arg Lys Phe Ala Arg Ser Asp Glu Arg Lys Arg His Thr Lys
405 410 415
atc cac ttg cgg cag aag gac aag aaa gac aca agt gtt gtg gcc 1296
Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
420 425 430
tct tcg gcc acc tcc tct ctc tct tcc tac ccg tcc ccg gtt gct acc 1344
Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
435 440 445
tct tac ccg tcc ccg gtt act acc tct tat cca tcc ccg gcc acc acc 1392
Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
450 455 460
tca tac cca tcc cct gtg ccc acc tcc ttc tcc tct ccc ggc tcc tcg 1440
Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
465 470 475 480
acc tac cca tcc cct gtg cac agt ggc ttc ccc tcc ccg tcg gtg gcc 1488
Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
485 490 495
acc acg tac tcc tct gtt ccc cct gct ttc ccg gcc cag gtc agc agc 1536
Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
500 505 510
ttc cct tcc tca gct gtc acc aac tcc ttc agc gcc tcc aca ggg ctt 1584
Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
515 520 525
tcg gac atg aca gca acc ttt tct ccc agg aca att gaa att tgc 1629
Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
530 535 540

```

<210> 4
 <211> 1629
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1629)
 <223>

```

<400> 4
atg gcc gcg gcc aag gcc gag atg cag ctg atg tcc ccg ctg cag atc 48
Met Ala Ala Ala Lys Ala Glu Met Gln Leu Met Ser Pro Leu Gln Ile
1 5 10 15
tct gac ccg ttc gga tcc ttt cct cac tcg ccc acc atg gac aac tac 96
Ser Asp Pro Phe Gly Ser Phe Pro His Ser Pro Thr Met Asp Asn Tyr
20 25 30
cct aag ctg gag gag atg atg ctg ctg agc aac ggg gct ccc cag ttc 144
Pro Lys Leu Glu Glu Met Met Leu Leu Ser Asn Gly Ala Pro Gln Phe
35 40 45
ctc ggc gcc gcc ggg gcc cca gag ggc agc ggc agc aac agc agc agc 192
Leu Gly Ala Ala Gly Ala Pro Glu Gly Ser Gly Ser Asn Ser Ser Ser
50 55 60
agc agc agc ggg ggc ggt gga ggc ggc ggg ggc ggc agc aac agc agc 240

```

04080seq.txt

Ser 65	Ser	Ser	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ser	Asn	Ser	Ser		
				70						75					80		
agc	agc	agc	agc	acc	ttc	aac	cct	cag	gcg	gac	acg	ggc	gag	cag	ccc	288	
Ser	Ser	Ser	Ser	Thr	Phe	Asn	Pro	Gln	Ala	Asp	Thr	Gly	Glu	Gln	Pro		
				85				90						95			
tac	gag	cac	ctg	acc	gca	gag	tct	ttt	cct	gac	atc	tct	ctg	aac	aac	336	
Tyr	Glu	His	Leu	Thr	Ala	Glu	Ser	Phe	Pro	Asp	Ile	Ser	Leu	Asn	Asn		
			100					105					110				
gag	aag	gtg	ctg	gtg	gag	acc	agt	tac	ccc	agc	caa	acc	act	cga	ctg	384	
Glu	Lys	Val	Leu	Val	Glu	Thr	Ser	Tyr	Pro	Ser	Gln	Thr	Thr	Arg	Leu		
		115					120					125					
ccc	ccc	atc	acc	tat	act	ggc	cgc	ttt	tcc	ctg	gag	cct	gca	ccc	aac	432	
Pro	Pro	Ile	Thr	Tyr	Thr	Gly	Arg	Phe	Ser	Leu	Glu	Pro	Ala	Pro	Asn		
		130				135			140								
agt	ggc	aac	acc	ttg	tgg	ccc	gag	ccc	ctc	ttc	agc	ttg	gtc	agt	ggc	480	
Ser	Gly	Asn	Thr	Leu	Trp	Pro	Glu	Pro	Leu	Phe	Ser	Leu	Val	Ser	Gly		
145				150				155							160		
cta	gtg	agc	atg	acc	aac	cca	ccg	gcc	tcc	tcg	tcc	tca	gca	cca	tct	528	
Leu	Val	Ser	Met	Thr	Asn	Pro	Pro	Ala	Ser	Ser	Ser	Ser	Ala	Pro	Ser		
			165					170					175				
cca	gcg	gcc	tcc	tcc	gcc	tcc	gcc	tcc	cag	agc	cca	ccc	ctg	agc	tgc	576	
Pro	Ala	Ala	Ser	Ser	Ala	Ser	Ala	Ser	Gln	Ser	Pro	Pro	Leu	Ser	Cys		
		180					185					190					
gca	gtg	cca	tcc	aac	gac	agc	agt	ccc	att	tac	tca	gcg	gca	ccc	acc	624	
Ala	Val	Pro	Ser	Asn	Asp	Ser	Ser	Pro	Ile	Tyr	Ser	Ala	Ala	Pro	Thr		
		195				200					205						
ttc	ccc	acg	ccg	aac	act	gac	att	ttc	cct	gag	cca	caa	agc	cag	gcc	672	
Phe	Pro	Thr	Pro	Asn	Thr	Asp	Ile	Phe	Pro	Glu	Pro	Gln	Ser	Gln	Ala		
	210					215			220								
ttc	ccg	ggc	tcg	gca	ggg	aca	gcg	ctc	cag	tac	ccg	cct	cct	gcc	tac	720	
Phe	Pro	Gly	Ser	Ala	Gly	Thr	Ala	Leu	Gln	Tyr	Pro	Pro	Pro	Ala	Tyr		
225				230				235						240			
cct	gcc	gcc	aag	ggg	ggc	ttc	cag	gtt	ccc	atg	atc	ccc	gac	tac	ctg	768	
Pro	Ala	Ala	Lys	Gly	Gly	Phe	Gln	Val	Pro	Met	Ile	Pro	Asp	Tyr	Leu		
			245					250					255				
ttt	cca	cag	cag	cag	ggg	gat	ctg	ggc	ctg	ggc	acc	cca	gac	cag	aag	816	
Phe	Pro	Gln	Gln	Gln	Gly	Asp	Leu	Gly	Leu	Gly	Thr	Pro	Asp	Gln	Lys		
		260					265					270					
ccc	ttc	cag	ggc	ctg	gag	agc	cgc	acc	cag	cag	cct	tcg	cta	acc	cct	864	
Pro	Phe	Gln	Gly	Leu	Glu	Ser	Arg	Thr	Gln	Gln	Pro	Ser	Leu	Thr	Pro		
		275					280				285						
ctg	tct	act	att	aag	gcc	ttt	gcc	act	cag	tcg	ggc	tcc	cag	gac	ctg	912	
Leu	Ser	Thr	Ile	Lys	Ala	Phe	Ala	Thr	Gln	Ser	Gly	Ser	Gln	Asp	Leu		
	290					295					300						
aag	gcc	ctc	aat	acc	agc	tac	cag	tcc	cag	ctc	atc	aaa	ccc	agc	cgc	960	
Lys	Ala	Leu	Asn	Thr	Ser	Tyr	Gln	Ser	Gln	Leu	Ile	Lys	Pro	Ser	Arg		
305				310				315						320			
atg	cgc	aag	tac	ccc	aac	cgg	ccc	agc	aag	acg	ccc	ccc	cac	gaa	cgc	1008	
Met	Arg	Lys	Tyr	Pro	Asn	Arg	Pro	Ser	Lys	Thr	Pro	Pro	His	Glu	Arg		
			325					330					335				
cct	tac	gct	tgc	cca	gtg	gag	tcc	tgt	gat	cgc	cgc	ttc	tcc	cgc	tcc	1056	
Pro	Tyr	Ala	Cys	Pro	Val	Glu	Ser	Cys	Asp	Arg	Arg	Phe	Ser	Arg	Ser		
		340					345					350					
gac	gag	ctc	acc	cgc	cac	atc	cgc	atc	cac	aca	ggc	cag	aag	ccc	ttc	1104	
Asp	Glu	Leu	Thr	Arg	His	Ile	Arg	Ile	His	Thr	Gly	Gln	Lys	Pro	Phe		
		355				360					365						
cag	tgc	cgc	atc	tgc	atg	cgc	aac	ttc	agc	cgc	agc	gac	cac	ctc	acc	1152	
Gln	Cys	Arg	Ile	Cys	Met	Arg	Asn	Phe	Ser	Arg	Ser	Asp	His	Leu	Thr		
		370				375					380						
acc	cac	atc	cgc	acc	cac	aca	ggc	gaa	aag	ccc	ttc	gcc	tgc	gac	atc	1200	
Thr	His	Ile	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Phe	Ala	Cys	Asp	Ile		
		385			390					395					400		
tgt	gga	aga	aag	ttt	gcc	agg	agc	gat	gaa	cgc	aag	agg	cat	acc	aag	1248	
Cys	Gly	Arg	Lys	Phe	Ala	Arg	Ser	Asp	Glu	Arg	Lys	Arg	His	Thr	Lys		

04080seq.txt

```

          405          410          415
atc cac ttg cgg cag aag gac aag aaa gca gac aaa agt gtt gtg gcc 1296
Ile His Leu Arg Gln Lys Asp Lys Lys Ala Asp Lys Ser Val Val Ala
          420          425          430
tct tcg gcc acc tcc tct ctc tct tcc tac ccg tcc ccg gtt gct acc 1344
Ser Ser Ala Thr Ser Ser Leu Ser Ser Tyr Pro Ser Pro Val Ala Thr
          435          440          445
tct tac ccg tcc ccg gtt act acc tct tat cca tcc ccg gcc acc acc 1392
Ser Tyr Pro Ser Pro Val Thr Thr Ser Tyr Pro Ser Pro Ala Thr Thr
          450          455          460
tca tac cca tcc cct gtg ccc acc tcc ttc tcc tct ccc ggc tcc tcg 1440
Ser Tyr Pro Ser Pro Val Pro Thr Ser Phe Ser Ser Pro Gly Ser Ser
          465          470          475          480
acc tac cca tcc cct gtg cac agt ggc ttc ccc tcc ccg tcg gtg gcc 1488
Thr Tyr Pro Ser Pro Val His Ser Gly Phe Pro Ser Pro Ser Val Ala
          485          490          495
acc acg tac tcc tct gtt ccc cct gct ttc ccg gcc cag gtc agc agc 1536
Thr Thr Tyr Ser Ser Val Pro Pro Ala Phe Pro Ala Gln Val Ser Ser
          500          505          510
ttc cct tcc tca gct gtc acc aac tcc ttc agc gcc tcc aca ggg ctt 1584
Phe Pro Ser Ser Ala Val Thr Asn Ser Phe Ser Ala Ser Thr Gly Leu
          515          520          525
tcg gac atg aca gca acc ttt tct ccc agg aca att gaa att tgc 1629
Ser Asp Met Thr Ala Thr Phe Ser Pro Arg Thr Ile Glu Ile Cys
          530          535          540

```

<210> 5

<211> 9

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as decoy for Egr-1.

<400> 5

gcgtgggcg

9

<210> 6

<211> 9

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as decoy for Egr-1.

<400> 6

gcgggggcg

9

<210> 7

<211> 20

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<223> Oligonucleotide designed to act as antisense DNA for Egr-1 mRNA.

<400> 7

gcggggtgca ggggcacact

20

<210> 8

<211> 30

<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Oligonucleotide designed to act as primer for amplifying Egr-1
cDNA.

<400> 8
ccgaattcag tggtccccgc gccccgcatg 30

<210> 9
<211> 29
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Oligonucleotide designed to act as primer for amplifying Egr-1
cDNA.

<400> 9
ggctcgagaa cctccatctg acctaagag 29

<210> 10
<211> 26
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Oligonucleotide designed to act as sense strand of double-stranded
DNA capable of binding with Egr-1.

<400> 10
tgactcgccc tcgccccgc gccggg 26

<210> 11
<211> 26
<212> DNA
<213> Artificial

<220>
<221> misc_feature
<223> Oligonucleotide designed to act as sense strand of double-stranded
DNA incapable of binding with Egr-1.

<400> 11
tgactcgccc tcgaccagc gccggg 26